SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA

<120> Method for achieving a pathogen resistance in
plants

<130> PF53687

<140>
<141>

<160> 36

<170> PatentIn Ver. 2.1

<210> 1
<211> 1890
<212> DNA
<213> Protaminobacter rubrum

<220>
<221> CDS
<222> (1)..(1887)
<223> coding for sucrose isomerase

<400> 1

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Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
1               5                   10                  15

tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg    96
Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
                20                  25                  30

ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg   144
Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
            35                  40                  45

aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc   192
Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
        50                  55                  60

aac gga gat ggc atc ggg gat att aac ggc atc ata gaa aaa tta gac   240
Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
65                  70                  75                  80

tat cta aaa gcc ttg ggg att gat gcc att tgg atc aac cca cat tat   288
Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95

gat tct ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa   336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
                100                 105                 110

atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct   384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
            115                 120                 125

gaa atg aaa aaa cgg aat atg cgg ttg atg att gat gtg gtc atc aac   432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
        130                 135                 140

cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag   480
His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145                 150                 155                 160

gat aat cct tat cgc ggc tat tat ttc tgg aaa gat gct aaa gaa ggg   528
Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                165                 170                 175
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cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa    576
Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180             185                 190

aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa    624
Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195             200             205

cag cct gac cta aac tgg gat aat ccc aaa gtc cgt caa gat ctt tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
210             215             220

gca atg tta cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgt ttt    720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240

gat acg gta gcg acc tac tca aaa att ccg gat ttc cca aat ctc acc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
            245             250             255

caa caa cag ctg aag aat ttt gca gcg gag tat acc aag ggc cct aat    816
Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
            260             265             270

att cat cgt tac gtc aat gaa atg aat aaa gag gtc ttg tct cat tac    864
Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
            275             280             285

gac att gcg act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
            290             295             300

ata aag ttc ttc gat cgc cgc cgt gat gag ctg aac att gca ttt acc    960
Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305             310             315             320

ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga    1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
            325             330             335

aaa gat tgg aaa ttg tcg caa ttc cgg cag atc atc gat aac gtt gac    1056
Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
            340             345             350

cgt act gca gga gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac    1104
Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
            355             360             365

gac aat ccg cgc gct gtc tcg cac ttt ggc gat gat gat cgc cca caa    1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Arg Pro Gln
            370             375             380

tgg cgt gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa    1200
Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln
385             390             395             400

cga gca aca cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat    1248
Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn
            405             410             415

tac ccg ttt aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt    1296
Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly
            420             425             430

ttt tgg cat gac tac gtt gag aca gga aag gtc aaa gcc gac gag ttc    1344
Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe
            435             440             445
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ttg caa aat gta cgc ctg acg agc agg gat aac agc cgg acg ccg ttc     1392
Leu Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe
    450             455             460

caa tgg gat ggg agc aaa aat gca gga ttc acg agc gga aaa cct tgg     1440
Gln Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp
465             470             475             480

ttc aag gtc aac cca aac tac cag gaa atc aat gca gta agt caa gtc     1488
Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val
            485             490             495

aca caa ccc gac tca gta ttt aac tat tat cgt cag ttg atc aag ata     1536
Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile
        500             505             510

agg cat gac atc ccg gca ctg acc tat ggt aca tac acc gat ttg gat     1584
Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp
        515             520             525

cct gca aat gat tcg gtc tac gcc tat aca cgc agc ctt ggg gcg gaa     1632
Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu
        530             535             540

aaa tat ctt gtt gtt gtt aac ttc aag gag caa atg atg aga tat aaa     1680
Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys
545             550             555             560

tta ccg gat aat tta tcc att gag aaa gtg att ata gac agc aac agc     1728
Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser
            565             570             575

aaa aac gtg gtg aaa aag aat gat tca tta ctc gag cta aaa cca tgg     1776
Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp
            580             585             590

cag tca ggg gtt tat aaa act aaa tca ata aat ctc ata gtc acg cca     1824
Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro
        595             600             605

aat aat gta aat ata ttg aaa cta tta aaa ccg gca ttt tat gcc ggt     1872
Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly
    610             615             620

ttt ttt agc gca aaa tag                                             1890
Phe Phe Ser Ala Lys
625
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<212> PRT
<213> Protaminobacter rubrum

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Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
            20                  25                  30

Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
            35                  40                  45

Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
        50                  55                  60

Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
 65                 70                  75                      80
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Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                    85   90   95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
                100   105   110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
            115   120   125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130   135   140

His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145   150   155   160

Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                165   170   175

Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
                180   185   190

Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195   200   205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210   215   220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225   230   235   240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
                245   250   255

Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
            260   265   270

Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
        275   280   285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
    290   295   300

Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305   310   315   320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
            325   330   335

Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
        340   345   350

Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
        355   360   365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Arg Pro Gln
    370   375   380

Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln
385   390   395   400

Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn
                405   410   415

Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly
            420   425   430

Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe
        435   440   445

Leu Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe
450   455   460

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Gln Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp
465             470             475             480

Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val
            485             490             495

Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile
            500             505             510

Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp
            515             520             525

Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu
    530             535             540

Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys
545             550             555             560

Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser
            565             570             575

Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp
            580             585             590

Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro
            595             600             605

Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly
    610             615             620

Phe Phe Ser Ala Lys
625
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<210> 3
<211> 1305
<212> DNA
<213> Erwinia rhapontici

<220>
<221> CDS
<222> (1)..(1305)
<223> coding for N-terminal fragment of sucrose
      isomerase

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atg tcc tct caa gga ttg aaa acg gct ntc gct att ttt ctt gca acc    48
Met Ser Ser Gln Gly Leu Lys Thr Ala Xaa Ala Ile Phe Leu Ala Thr
 1               5               10                  15

act ttt tct gcc aca tcc tat cag gcc tgc agt gcc nnn cca gat acc    96
Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Xaa Pro Asp Thr
            20              25                  30

gcc ccc tca ctc acc gtt cag caa tca aat gcc ctg ccc aca tgg tgg   144
Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp
            35              40                  45

aag cag gct gtt ttt tat cag gta tat cca cgc tca ttt aaa gat acg   192
Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50              55                  60

aat ggg gat ggc att ggg gat tta aac ggt att att gag aat tta gac   240
Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp
65                  70                  75                  80

tat ctg aag aaa ctg ggt att gat gcg att tgg atc aat cca cat tac   288
Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95
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gat tcg ccg aat acg gat aat ggt tat gac atc cgg gat tac cgt aag    336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100                 105                 110

ata atg aaa gaa tac ggt acg atg gaa gac ttt gac cgt ctt att tca    384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
            115                 120                 125

gaa atg aag aaa cgc aat atg cgt ttg atg att gat att gtt atc aac    432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Ile Val Ile Asn
            130                 135                 140

cac acc agc gat cag cat gcc tgg ttt gtt cag agc aaa tcg ggt aag    480
His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser Lys Ser Gly Lys
145                 150                 155                 160

aac aac ccc tac agg gac tat tac ttc tgg cgt gac ggt aag gat ggc    528
Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly
                165                 170                 175

cat gcc ccc aat aac tat ccc tcc ttc ttc ggt ggc tca gcc tgg gaa    576
His Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu
                180                 185                 190

aaa gac gat aaa tca ggc cag tat tac ctc cat tac ttt gcc aaa cag    624
Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
                195                 200                 205

caa ccc gac ctc aac tgg gac aat ccc aaa gtc cgt caa gac ctg tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
            210                 215                 220

gac atg ctc cgc ttc tgg tta gat aaa ggc gtt tct ggt tta cgc ttt    720
Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225                 230                 235                 240

gat acc gtt gcc acc tac tcg aaa atc ccg aac ttc cct gac ctt agc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser
                245                 250                 255

caa cag cag tta aaa aat ttc gcc gag gaa tat act aaa ggt cct aaa    816
Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys
                260                 265                 270

att cac gac tac gtg aat gaa atg aac aga gaa gta tta tcc cac tat    864
Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
                275                 280                 285

gat atc gcc act gcg ggg gaa ata ttt ggg gtt cct ctg gat aaa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser
            290                 295                 300

att aag ttt ttc gat cgc cgt aga aat gaa tta aat ata gcg ttt acg    960
Ile Lys Phe Phe Asp Arg Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr
305                 310                 315                 320

ttt gat ctg atc agg ctc gat cgt gat gct gat gaa aga tgg cgg cga   1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg
                325                 330                 335

aaa gac tgg acc ctt tcg cag ttc cga aaa att gtc gat aag gtt gac   1056
Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp
                340                 345                 350

caa acg gca gga gag tat ggg tgg aat gcc ttt ttc tta gac aat cac   1104
Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
                355                 360                 365
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gac aat ccc cgc gcg gtt tct cac ttt ggt gat gat cga cca caa tgg   1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370                 375             380

cgc gag cat gcg gcg aaa gca ctg gca aca ttg acg ctg acc cag cgt   1200
Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385                 390             395                 400

gca acg ccg ttt atc tat cag ggt tca gaa ctc ggt atg acc aat tat   1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410                 415

ccc ttt aaa aaa atc gat gat ttc gat gat gta gag gtg aaa ggt ttt   1296
Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe
            420             425             430

tgg caa gac                                                       1305
Trp Gln Asp
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<210> 4
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<212> PRT
<213> Erwinia rhapontici

<400> 4

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Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Xaa Pro Asp Thr
            20              25              30

Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp
        35              40              45

Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50              55              60

Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp
65              70              75              80

Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
            85              90              95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100             105             110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
    115             120             125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Ile Val Ile Asn
    130             135             140

His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser Lys Ser Gly Lys
145             150             155             160

Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly
            165             170             175

His Ala Pro Asn Asn Tyr Pro Ser Phe Gly Gly Ser Ala Trp Glu
            180             185             190

Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
        195             200             205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210             215             220

Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240
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●   ●

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser
              245   250   255

Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys
          260   265   270

Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
          275   280   285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser
      290   295   300

Ile Lys Phe Phe Asp Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr
305   310   315   320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg
              325   330   335

Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp
          340   345   350

Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
          355   360   365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
      370   375   380

Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385   390   395   400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
              405   410   415

Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe
          420   425   430

Trp Gln Asp
      435

<210> 5
<211> 1803
<212> DNA
<213> Erwinia rhapontici

<220>
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<222> (1)..(1800)
<223> coding for sucrose isomerase

<400> 5
atg tcc tct caa gga ttg aaa acg gct gtc gct att ttt ctt gca acc   48
Met Ser Ser Gln Gly Leu Lys Thr Ala Val Ala Ile Phe Leu Ala Thr
 1   5   10   15

act ttt tct gcc aca tcc tat cag gcc tgc agt gcc ggg cca gat acc   96
Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Gly Pro Asp Thr
              20   25   30

gcc ccc tca ctc acc gtt cag caa tca aat gcc ctg ccc aca tgg tgg   144
Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp
          35   40   45

aag cag gct gtt ttt tat cag gta tat cca cgc tca ttt aaa gat acg   192
Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
          50   55   60

aat ggg gat ggc att ggg gat tta aac ggt att att gag aat tta gac   240
Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp
 65   70   75   80

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tat ctg aag aaa ctg ggt att gat gcg att tgg atc aat cca cat tac    288
Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
            85              90                  95

gat tcg ccg aat acg gat aat ggt tat gac atc cgg gat tac cgt aag    336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100             105             110

ata atg aaa gaa tac ggt acg atg gaa gac ttt gac cgt ctt att tca    384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
            115             120             125

gaa atg aag aaa cgc aat atg cgt ttg atg att gat att gtt atc aac    432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Ile Val Ile Asn
            130             135             140

cac acc agc gat cag cat gcc tgg ttt gtt cag agc aaa tcg ggt aag    480
His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser Lys Ser Gly Lys
145             150             155             160

aac aac ccc tac agg gac tat tac ttc tgg cgt gac ggt aag gat ggc    528
Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly
            165             170             175

cat gcc ccc aat aac tat ccc tcc ttc ttc ggt ggc tca gcc tgg gaa    576
His Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu
            180             185             190

aaa gac gat aaa tca ggc cag tat tac ctc cat tac ttt gcc aaa cag    624
Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195             200             205

caa ccc gac ctc aac tgg gac aat ccc aaa gtc cgt caa gac ctg tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
            210             215             220

gac atg ctc cgc ttc tgg tta gat aaa ggc gtt tct ggt tta cgc ttt    720
Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240

gat acc gtt gcc acc tac tcg aaa atc ccg aac ttc cct gac ctt agc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser
            245             250             255

caa cag cag tta aaa aat ttc gcc gag gaa tat act aaa ggt cct aaa    816
Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys
            260             265             270

att cac gac tac gtg aat gaa atg aac aga gaa gta tta tcc cac tat    864
Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
            275             280             285

gat atc gcc act gcg ggg gaa ata ttt ggg gtt cct ctg gat aaa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser
            290             295             300

att aag ttt ttc gat cgc cgt aga aat gaa tta aat ata gcg ttt acg    960
Ile Lys Phe Phe Asp Arg Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr
305             310             315             320

ttt gat ctg atc agg ctc gat cgt gat gct gat gaa aga tgg cgg cga    1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg
            325             330             335

aaa gac tgg acc ctt tcg cag ttc cga aaa att gtc gat aag gtt gac    1056
Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp
            340             345             350
```

```
caa acg gca gga gag tat ggg tgg aat gcc ttt ttc tta gac aat cac    1104
Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
        355             360             365

gac aat ccc cgc gcg gtt tct cac ttt ggt gat gat cga cca caa tgg    1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370             375             380

cgc gag cat gcg gcg aaa gca ctg gca aca ttg acg ctg acc cag cgt    1200
Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385             390             395             400

gca acg ccg ttt atc tat cag ggt tca gaa ctc ggt atg acc aat tat    1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410             415

ccc ttt aaa aaa atc gat gat ttc gat gat gta gag gtg aaa ggt ttt    1296
Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe
            420             425             430

tgg caa gac tac gtt gaa aca ggc aaa gtg aaa gct gag gaa ttc ctt    1344
Trp Gln Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Glu Glu Phe Leu
            435             440             445

caa aac gta cgc caa acc agc cgt gat aac agc aga acc ccc ttc cag    1392
Gln Asn Val Arg Gln Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450             455             460

tgg gat gca agc aaa aac gcg ggc ttt acc agt gga acc ccc tgg tta    1440
Trp Asp Ala Ser Lys Asn Ala Gly Phe Thr Ser Gly Thr Pro Trp Leu
465             470             475             480

aaa atc aat ccc aat tat aaa gaa atc aac agc gca gat cag att aat    1488
Lys Ile Asn Pro Asn Tyr Lys Glu Ile Asn Ser Ala Asp Gln Ile Asn
                485             490             495

aat cca aat tcc gta ttt aac tat tat aga aag ctg att aac att cgc    1536
Asn Pro Asn Ser Val Phe Asn Tyr Tyr Arg Lys Leu Ile Asn Ile Arg
            500             505             510

cat gac atc cct gcc ttg acc tac ggc agt tat att gat tta gac cct    1584
His Asp Ile Pro Ala Leu Thr Tyr Gly Ser Tyr Ile Asp Leu Asp Pro
        515             520             525

gac aac aat tca gtc tat gct tac acc cga acg ctc ggc gct gaa aaa    1632
Asp Asn Asn Ser Val Tyr Ala Tyr Thr Arg Thr Leu Gly Ala Glu Lys
    530             535             540

tat ctt gtg gtc att aat ttt aaa gaa gaa gtg atg cac tac acc ctg    1680
Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met His Tyr Thr Leu
545             550             555             560

ccc ggg gat tta tcc atc aat aag gtg att act gaa aac aac agt cac    1728
Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu Asn Asn Ser His
                565             570             575

act att gtg aat aaa aat gac agg caa ctc cgt ctt gaa ccc tgg cag    1776
Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu Glu Pro Trp Gln
            580             585             590

tcg ggc att tat aaa ctt aat ccg tag                                1803
Ser Gly Ile Tyr Lys Leu Asn Pro
        595             600
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<210> 6
<211> 600
<212> PRT
<213> Erwinia rhapontici

<400> 6

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Met Ser Ser Gln Gly Leu Lys Thr Ala Val Ala Ile Phe Leu Ala Thr
1               5               10              15

Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Gly Pro Asp Thr
          20              25              30

Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp
          35              40              45

Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50              55              60

Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp
65              70              75              80

Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
              85              90              95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
          100             105             110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
    115             120             125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Ile Val Ile Asn
    130             135             140

His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser Lys Ser Gly Lys
145             150             155             160

Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly
          165             170             175

His Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu
          180             185             190

Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
    195             200             205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210             215             220

Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser
              245             250             255

Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys
          260             265             270

Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
    275             280             285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser
290             295             300

Ile Lys Phe Phe Asp Arg Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr
305             310             315             320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg
              325             330             335

Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp
          340             345             350

Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
          355             360             365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370             375             380
```

```
Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385             390             395                     400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410                 415

Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe
            420             425                 430

Trp Gln Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Glu Glu Phe Leu
        435             440                 445

Gln Asn Val Arg Gln Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
    450                 455                 460

Trp Asp Ala Ser Lys Asn Ala Gly Phe Thr Ser Gly Thr Pro Trp Leu
465             470                 475                     480

Lys Ile Asn Pro Asn Tyr Lys Glu Ile Asn Ser Ala Asp Gln Ile Asn
            485                 490                 495

Asn Pro Asn Ser Val Phe Asn Tyr Tyr Arg Lys Leu Ile Asn Ile Arg
            500                 505                 510

His Asp Ile Pro Ala Leu Thr Tyr Gly Ser Tyr Ile Asp Leu Asp Pro
            515             520                 525

Asp Asn Asn Ser Val Tyr Ala Tyr Thr Arg Thr Leu Gly Ala Glu Lys
    530                 535                 540

Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met His Tyr Thr Leu
545             550                 555                     560

Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu Asn Asn Ser His
            565                 570                 575

Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu Glu Pro Trp Gln
            580                 585                 590

Ser Gly Ile Tyr Lys Leu Asn Pro
        595                 600
```

<210> 7
<211> 1803
<212> DNA
<213> Protaminobacter rubrum

<220>
<221> CDS
<222> (1)..(1800)
<223> coding for sucrose isomerase

<400> 7

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atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca    48
Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
 1               5                  10                  15

tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg    96
Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
            20                  25                  30

ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg   144
Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
        35                  40                  45

aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc   192
Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50                  55                  60
```

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aac gga gat ggc atc ggg gat att aac ggc atc ata gaa aaa tta gac    240
Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
 65              70                  75                  80

tat cta aaa gcc ttg ggg att gat gcc att tgg atc aac cca cat tat    288
Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95

gat tct ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa    336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100                 105                 110

atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct    384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
        115                 120                 125

gaa atg aaa aaa cgg aat atg cgg ttg atg att gat gtg gtc atc aac    432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
        130                 135                 140

cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag    480
His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145                 150                 155                 160

gat aat cct tat cgc ggc tat tat ttc tgg aaa gat gct aaa gaa ggg    528
Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                165                 170                 175

cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa    576
Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180                 185                 190

aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa    624
Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195                 200                 205

cag cct gac cta aac tgg gat aat ccc aaa gtc cgt caa gat ctt tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
        210                 215                 220

gca atg tta cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgt ttt    720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225                 230                 235                 240

gat acg gta gcg acc tac tca aaa att ccg gat ttc cca aat ctc acc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
                245                 250                 255

caa caa cag ctg aag aat ttt gca gcg gag tat acc aag ggc cct aat    816
Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
            260                 265                 270

att cat cgt tac gtc aat gaa atg aat aaa gag gtc ttg tct cat tac    864
Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
            275                 280                 285

gac att gcg act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
        290                 295                 300

ata aag ttc ttc gat cgc cgc cgt gat gag ctg aac att gca ttt acc    960
Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305                 310                 315                 320

ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga   1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
                325                 330                 335
```

```
aaa gat tgg aaa ttg tcg caa ttc cgg cag atc atc gat aac gtt gac    1056
Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
            340             345             350

cgt act gca gga gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac    1104
Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
            355             360             365

gac aat ccg cgc gct gtc tcg cac ttt ggc gat gat cgc cca caa tgg    1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
        370             375             380

cgt gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa cga    1200
Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385             390             395             400

gca aca cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat tac    1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410             415

ccg ttt aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt ttt    1296
Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
                420             425             430

tgg cat gac tac gtt gag aca gga aag gtc aaa gcc gac gag ttc ttg    1344
Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
            435             440             445

caa aat gta cgc ctg acg agc agg gat aac agc cgg acg ccg ttc caa    1392
Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450             455             460

tgg gat ggg agc aaa aat gca gga ttc acg agc gga aaa cct tgg ttc    1440
Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465             470             475             480

aag gtc aac cca aac tac cag gaa atc aat gca gta agt caa gtc aca    1488
Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Thr
                485             490             495

caa ccc gac tca gta ttt aac tat tat cgt cag ttg atc aag ata agg    1536
Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
                500             505             510

cat gac atc ccg gca ctg acc tat ggt aca tac acc gat ttg gat cct    1584
His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
                515             520             525

gca aat gat tcg gtc tac gcc tat aca cgc agc ctt ggg gcg gaa aaa    1632
Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
        530             535             540

tat ctt gtt gtt gtt aac ttc aag gag caa atg atg aga tat aaa tta    1680
Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys Leu
545             550             555             560

ccg gat aat tta tcc att gag aaa gtg att ata gac agc aac agc aaa    1728
Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser Lys
            565             570             575

aac gtg gtg aaa aag aat gat tca tta ctc gag cta aaa cca tgg cag    1776
Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
            580             585             590

tca ggg gtt tat aaa cta aat caa taa                                1803
Ser Gly Val Tyr Lys Leu Asn Gln
            595             600
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<210> 8
<211> 600
<212> PRT
<213> Protaminobacter rubrum

<400> 8

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Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
1               5               10              15

Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu
            20              25              30

Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
        35              40              45

Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50              55              60

Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp
65              70              75              80

Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
            85              90              95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
        100             105             110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
        115             120             125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130             135             140

His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145             150             155             160

Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
            165             170             175

Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
        180             185             190

Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
        195             200             205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210             215             220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
            245             250             255

Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
        260             265             270

Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr
        275             280             285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
    290             295             300

Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305             310             315             320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
            325             330             335

Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp
            340             345             350
```

```
Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
        355                 360                 365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
        370                 375                 380

Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385                 390                 395                 400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405                 410                 415

Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
                420                 425                 430

Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
        435                 440                 445

Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450                 455                 460

Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465                 470                 475                 480

Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Thr
                485                 490                 495

Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
                500                 505                 510

His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
        515                 520                 525

Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
        530                 535                 540

Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys Leu
545                 550                 555                 560

Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser Lys
                565                 570                 575

Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
                580                 585                 590

Ser Gly Val Tyr Lys Leu Asn Gln
        595                 600


<210> 9
<211> 1794
<212> DNA
<213> Enterobacter sp.

<220>
<221> CDS
<222> (1)..(1791)
<223> coding for sucrose isomerase

<400> 9
atg tct ttt gtt acg cta cgt acc ggg gtg gct gtc gcg ctg tca tct    48
Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser
 1               5                  10                  15

ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg    96
Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu
            20                  25                  30

aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg   144
Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp
            35                  40                  45
```

```
aaa gaa gct gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc    192
Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr
    50              55                  60

aat gat gat ggc att ggc gat att cgc ggt att att gaa aag ctg gac    240
Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp
65          70                  75                      80

tat ctg aaa tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac    288
Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95

gac tct ccg aac acc gat aac ggc tat gac atc agt aat tat cgt cag    336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
            100                 105                 110

ata atg aaa gag tat ggc aca atg gag gat ttt gat agc ctt gtt gcc    384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala
            115                 120                 125

gaa atg aaa aaa cga aat atg cgc tta atg atc gac gtg gtc att aac    432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
        130                 135                 140

cat acc agt gat caa cac ccg tgg ttt att cag agt aaa agc gat aaa    480
His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
145                 150                 155                 160

aac aac cct tat cgt gac tat tat ttc tgg cgt gac gga aaa gat aat    528
Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn
                165                 170                 175

cag cca cct aat aat tac ccc tca ttt ttc ggc ggc tcg gca tgg caa    576
Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180                 185                 190

aaa gat gca aag tca gga cag tac tat tta cac tat ttt gcc aga cag    624
Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
            195                 200                 205

caa cct gat ctc aac tgg gat aac ccg aaa gta cgt gag gat ctt tac    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr
    210                 215                 220

gca atg ctc cgc ttc tgg ctg gat aaa ggc gtt tca ggc atg cga ttt    720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe
225                 230                 235                 240

gat acg gtg gca act tat tcc aaa atc ccg gga ttt ccc aat ctg aca    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr
                245                 250                 255

cct gaa caa cag aaa aat ttt gct gaa caa tac acc atg ggd cct aat    816
Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Xaa Pro Asn
            260                 265                 270

att cat cga tac att cag gaa atg aac cgg aaa gtt ctg tcc cgg tat    864
Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr
            275                 280                 285

gat gtg gcc acc gcg ggt gaa att ttt ggc gtc ccg ctg gat cgt tcg    912
Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser
            290                 295                 300

tcg cag ttt ttt gat cgc cgc cga cat gag ctg aat atg gcg ttt atg    960
Ser Gln Phe Phe Asp Arg Arg Arg His Glu Leu Asn Met Ala Phe Met
305                 310                 315                 320
```

● ●

```
ttt gac ctc att cgt ctc gat cgc gac agc aat gaa cgc tgg cgt cac   1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His
            325             330             335

aag tcg tgg tcg ctc tct cag ttc cgc cag atc atc agc aaa atg gat   1056
Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp
            340             345             350

gtc acg gtc gga aag tat ggc tgg aac acg ttc ttc tta gac aac cat   1104
Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His
            355             360             365

gac aac ccc cgt gcg gta tct cac ttc ggg gat gac agg ccg caa tgg   1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370             375             380

cgg gag gcg tcg gct aag gca ctg gcg acg att acc ctc act cag cgg   1200
Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg
385             390             395             400

gcg acg ccg ttt att tat cag ggt tca gag ctg gga atg act aat tat   1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410             415

ccc ttc agg caa ctc aac gaa ttt gac gac atc gag gtc aaa ggt ttc   1296
Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420             425             430

tgg cag gat tat gtc cag agt gga aaa gtc acg gcc aca gag ttt ctc   1344
Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu
            435             440             445

gat aat gtg cgc ctg acg agc cgc gat aac agc aga aca cct ttc cag   1392
Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
    450             455             460

tgg aat gac acc ctg aat gct ggt ttt act cgc gga aag ccg tgg ttt   1440
Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe
465             470             475             480

cac atc aac cca aac tat gtg gag atc aac scc gaa cgc gaa gaa acc   1488
His Ile Asn Pro Asn Tyr Val Glu Ile Asn Xaa Glu Arg Glu Glu Thr
            485             490             495

cgc gaa gat tca gtg ctg aat tac tat aaa aaa atg att cag cta cgc   1536
Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg
            500             505             510

cac cat atc cct gct ctg gta tat ggc gcc tat cag gat ctt aat cca   1584
His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro
            515             520             525

cag gac aat acc gtt tat gcc tat acc cga acg ctg ggt aac gag cgt   1632
Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg
    530             535             540

tat ctg gtc gtg gtg aac ttt aag gag tac ccg gtc cgc tat act ctc   1680
Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu
545             550             555             560

ccg gct aat gat gcc atc gag gaa gtg gtc att gat act cag cag caa   1728
Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln
                565             570             575

ggt gcg ccg cac agc aca tcc ctg tca ttg agc ccc tgg cag gca ggt   1776
Gly Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala Gly
            580             585             590
```

```
gcg tat aag ctg cgg taa                                              1794
Ala Tyr Lys Leu Arg
        595

<210> 10
<211> 597
<212> PRT
<213> Enterobacter sp.

<400> 10
Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser
 1               5                  10                  15

Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu
                 20                  25                  30

Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp
            35                  40                  45

Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr
        50                  55                  60

Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp
65                  70                  75                  80

Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
            100                 105                 110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala
            115                 120                 125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130                 135                 140

His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
145                 150                 155                 160

Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn
                165                 170                 175

Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180                 185                 190

Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
        195                 200                 205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr
    210                 215                 220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe
225                 230                 235                 240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr
                245                 250                 255

Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Xaa Pro Asn
            260                 265                 270

Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr
            275                 280                 285

Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser
        290                 295                 300

Ser Gln Phe Phe Asp Arg Arg Arg His Glu Leu Asn Met Ala Phe Met
305                 310                 315                 320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His
                325                 330                 335
```

```
Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp
        340             345                 350

Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His
        355                 360                 365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
        370                 375                 380

Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg
385                 390                 395                 400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405                 410                 415

Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420                 425                 430

Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu
            435                 440                 445

Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450                 455                 460

Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe
465                 470                 475                 480

His Ile Asn Pro Asn Tyr Val Glu Ile Asn Xaa Glu Arg Glu Glu Thr
                485                 490                 495

Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg
            500                 505                 510

His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro
            515                 520                 525

Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg
        530                 535                 540

Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu
545                 550                 555                 560

Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln
                565                 570                 575

Gly Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala Gly
            580                 585                 590

Ala Tyr Lys Leu Arg
            595
```

<210> 11
<211> 1803
<212> DNA
<213> Serratia plymuthica

<220>
<221> CDS
<222> (1)..(1800)
<223> coding for sucrose isomerase

<400> 11

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atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca    48
Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
 1               5                  10                  15

tca tta agc gtc tca tgc cag caa gcc tta ggt acg caa caa ccc ttg    96
Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu
            20                  25                  30
```

```
ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg    144
Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
         35              40                  45

aag gag gct gtt ttt tat cag gtg tat ccg cgt tcc ttt aaa gac act    192
Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
     50              55                  60

aac ggg gat ggt atc ggg gat att aaa ggc atc ata gaa aaa tta gac    240
Asn Gly Asp Gly Ile Gly Asp Ile Lys Gly Ile Ile Glu Lys Leu Asp
 65              70                  75                  80

tat tta aaa gct ttg ggg att gat gcc att tgg atc aac cca cat tat    288
Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                 85                  90                  95

gac tcc ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa    336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
             100                 105                 110

atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct    384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
         115                 120                 125

gaa atg aaa aaa cgt aac atg cgg ttg atg att gat gtg gtc atc aac    432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
         130                 135                 140

cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag    480
His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145                 150                 155                 160

gat aat cct tat cgt ggc tat tac ttc tgg aaa gat gct aaa gaa ggg    528
Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                 165                 170                 175

cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa    576
Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
             180                 185                 190

aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa    624
Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
         195                 200                 205

cag cct gac cta aac tgg gat aac ccc aaa gtc cgt caa gat ctt tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
     210                 215                 220

gca atg ttg cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgc ttt    720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225                 230                 235                 240

gat acg gta gcg acc tac tca aaa att ccg gac ttc cca aat ctc acc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
             245                 250                 255

caa caa cag ctg aag aat ttt gca gct gag tat acc aag ggc cct aat    816
Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
             260                 265                 270

att cat cgt tac gtc aat gaa atg aat aga gaa gtt ttg tct cat tac    864
Ile His Arg Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
         275                 280                 285

gac att gcc act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
         290                 295                 300
```

```
ata aaa ttc ttc gat cgc cgt cgc gat gag ctg aac atc gca ttt acc    960
Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305             310             315             320

ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga   1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
                325             330             335

aaa gag tgg aaa ttg tcg caa ttc cga cag gtc atc gat aac gtt gac   1056
Lys Glu Trp Lys Leu Ser Gln Phe Arg Gln Val Ile Asp Asn Val Asp
            340             345             350

cgt act gcc ggc gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac   1104
Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
            355             360             365

gac aat ccg cgc gct gtc tcc cac ttt ggc gat gat cgc cca caa tgg   1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
        370             375             380

cgc gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa cga   1200
Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385             390             395             400

gca acg cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat tac   1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
                405             410             415

ccc ttc aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt ttt   1296
Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
                420             425             430

tgg cat gac tac gtt gag aca gga aag gtg aaa gcc gac gag ttc ttg   1344
Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
            435             440             445

caa aat gta cgc ctg acg agc agg gat aac agc cgg aca ccg ttc caa   1392
Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450             455             460

tgg gat acg agc aaa aat gca gga ttc acg agc gga aaa cct tgg ttc   1440
Trp Asp Thr Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465             470             475             480

aag gtc aat cca aac tac cag gaa atc aat gcg gta agt caa gtc gca   1488
Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Ala
                485             490             495

cag ccc gac tcg gta ttt aat tat tat cgt cag ttg atc aag ata agg   1536
Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
            500             505             510

cat aac atc ccg gca ctg acc tat ggc aca tac acc gat ttg gat cct   1584
His Asn Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
            515             520             525

gca aat gat tcg gtc tac gcc tat aca cgc agc ctt ggg gcg gaa aaa   1632
Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
        530             535             540

tat ctt gtt gtc gtt aac ttc cag gaa caa gtg atg aga tat aaa tta   1680
Tyr Leu Val Val Val Asn Phe Gln Glu Gln Val Met Arg Tyr Lys Leu
545             550             555             560

ccg gat aat cta tcc atc gag aaa gtg att ata gaa agc aac agc aaa   1728
Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys
            565             570             575
```

```
aac gtt gtg aaa aag aat gat tcc tta ctc gaa cta aaa cca tgg cag    1776
Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
            580             585                 590

tca ggg gtt tat aaa cta aat caa taa                                1803
Ser Gly Val Tyr Lys Leu Asn Gln
            595             600
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<210> 12
<211> 600
<212> PRT
<213> Serratia plymuthica

<400> 12

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Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
 1               5                  10                     15

Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu
            20              25                  30

Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
            35              40                  45

Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
        50              55                  60

Asn Gly Asp Gly Ile Gly Asp Ile Lys Gly Ile Ile Glu Lys Leu Asp
65                  70                  75                  80

Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
            85                  90                  95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100             105                 110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
        115             120                 125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130             135                 140

His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145             150             155                 160

Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
            165                 170                 175

Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180             185                 190

Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195                 200             205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210             215                 220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230                 235                 240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
            245                 250                 255

Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
            260             265                 270

Ile His Arg Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
            275             280                 285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
290                 295                 300
```

Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305   310   315   320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
            325   330   335

Lys Glu Trp Lys Leu Ser Gln Phe Arg Gln Val Ile Asp Asn Val Asp
            340   345   350

Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
        355   360   365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370   375   380

Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385   390   395   400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
            405   410   415

Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
        420   425   430

Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
        435   440   445

Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
    450   455   460

Trp Asp Thr Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465   470   475   480

Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Ala
            485   490   495

Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
            500   505   510

His Asn Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
        515   520   525

Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
    530   535   540

Tyr Leu Val Val Val Asn Phe Gln Glu Gln Val Met Arg Tyr Lys Leu
545   550   555   560

Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys
            565   570   575

Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
            580   585   590

Ser Gly Val Tyr Lys Leu Asn Gln
        595   600

<210> 13
<211> 1844
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: coding for
      fusion protein of signal peptide from proteinase
      inhibitor I and sucrose isomerase from Erwinia
      rhapontici

<220>
<221> CDS
<222> (24)..(1835)

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<220>
<221> sig_peptide
<222> (24)..(143)
<223> signal peptide from proteinase inhibitor I

<220>
<221> misc_feature
<222> (144)..(1835)
<223> coding for mature peptide of sucrose isomerase
      from Erwinia rhapontici    (palI)

<400> 13
ggtaccctaa ttaattatcc atc atg gat gtt cac aag gaa gtt aat ttc gtt   53
                          Met Asp Val His Lys Glu Val Asn Phe Val
                           1           5                       10

gct tac cta cta att gtt ctt gga tta ttg gta ctt gta agc gcg atg   101
Ala Tyr Leu Leu Ile Val Leu Gly Leu Leu Val Leu Val Ser Ala Met
                15                  20                  25

gag cat gtt gat gcg aag gct tgc acc gaa ttg ggg atc ctc acc gtt   149
Glu His Val Asp Ala Lys Ala Cys Thr Glu Leu Gly Ile Leu Thr Val
                30                  35                  40

cag caa tca aat gcc ctg ccc aca tgg tgg aag cag gct gtt ttt tat   197
Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp Lys Gln Ala Val Phe Tyr
                45                  50                  55

cag gta tat cca cgc tca ttt aaa gat acg aat ggg gat ggc att ggg   245
Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly
         60                  65                  70

gat tta aac ggt att att gag aat tta gac tat ctg aag aaa ctg ggt   293
Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp Tyr Leu Lys Lys Leu Gly
 75                  80                  85                  90

att gat gcg att tgg atc aat cca cat tac gat tcg ccg aat acg gat   341
Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp
                95                  100                 105

aat ggt tat gac atc cgg gat tac cgt aag ata atg aaa gaa tac ggt   389
Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys Ile Met Lys Glu Tyr Gly
                110                 115                 120

acg atg gaa gac ttt gac cgt ctt att tca gaa atg aag aaa cgc aat   437
Thr Met Glu Asp Phe Asp Arg Leu Ile Ser Glu Met Lys Lys Arg Asn
                125                 130                 135

atg cgt ttg atg att gat att gtt atc aac cac acc agc gat cag cat   485
Met Arg Leu Met Ile Asp Ile Val Ile Asn His Thr Ser Asp Gln His
                140                 145                 150

gcc tgg ttt gtt cag agc aaa tcg ggt aag aac aac ccc tac agg gac   533
Ala Trp Phe Val Gln Ser Lys Ser Gly Lys Asn Asn Pro Tyr Arg Asp
155                 160                 165                 170

tat tac ttc tgg cgt gac ggt aag gat ggc cat gcc ccc aat aac tat   581
Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly His Ala Pro Asn Asn Tyr
                175                 180                 185

ccc tcc ttc ttc ggt ggc tca gcc tgg gaa aaa gac gat aaa tca ggc   629
Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu Lys Asp Asp Lys Ser Gly
                190                 195                 200

cag tat tac ctc cat tac ttt gcc aaa cag caa ccc gac ctc aac tgg   677
Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln Gln Pro Asp Leu Asn Trp
                205                 210                 215
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● ●

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gac aat ccc aaa gtc cgt caa gac ctg tat gac atg ctc cgc ttc tgg    725
Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr Asp Met Leu Arg Phe Trp
220             225             230

tta gat aaa ggc gtt tct ggt tta cgc ttt gat acc gtt gcc acc tac    773
Leu Asp Lys Gly Val Ser Gly Leu Arg Phe Asp Thr Val Ala Thr Tyr
235             240             245             250

tcg aaa atc ccg aac ttc cct gac ctt agc caa cag cag tta aaa aat    821
Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser Gln Gln Gln Leu Lys Asn
                255             260             265

ttc gcc gag gaa tat act aaa ggt cct aaa att cac gac tac gtg aat    869
Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys Ile His Asp Tyr Val Asn
            270             275             280

gaa atg aac aga gaa gta tta tcc cac tat gat atc gcc act gcg ggg    917
Glu Met Asn Arg Glu Val Leu Ser His Tyr Asp Ile Ala Thr Ala Gly
        285             290             295

gaa ata ttt ggg gtt cct ctg gat aaa tcg att aag ttt ttc gat cgc    965
Glu Ile Phe Gly Val Pro Leu Asp Lys Ser Ile Lys Phe Phe Asp Arg
    300             305             310

cgt aga aat gaa tta aat ata gcg ttt acg ttt gat ctg atc agg ctc   1013
Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr Phe Asp Leu Ile Arg Leu
315             320             325             330

gat cgt gat gct gat gaa aga tgg cgg cga aaa gac tgg acc ctt tcg   1061
Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg Lys Asp Trp Thr Leu Ser
            335             340             345

cag ttc cga aaa att gtc gat aag gtt gac caa acg gca gga gag tat   1109
Gln Phe Arg Lys Ile Val Asp Lys Val Asp Gln Thr Ala Gly Glu Tyr
            350             355             360

ggg tgg aat gcc ttt ttc tta gac aat cac gac aat ccc cgc gcg gtt   1157
Gly Trp Asn Ala Phe Phe Leu Asp Asn His Asp Asn Pro Arg Ala Val
        365             370             375

tct cac ttt ggt gat gat cga cca caa tgg cgc gag cat gcg gcg aaa   1205
Ser His Phe Gly Asp Asp Arg Pro Gln Trp Arg Glu His Ala Ala Lys
        380             385             390

gca ctg gca aca ttg acg ctg acc cag cgt gca acg ccg ttt atc tat   1253
Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg Ala Thr Pro Phe Ile Tyr
395             400             405             410

cag ggt tca gaa ctc ggt atg acc aat tat ccc ttt aaa aaa atc gat   1301
Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr Pro Phe Lys Lys Ile Asp
            415             420             425

gat ttc gat gat gta gag gtg aaa ggt ttt tgg caa gac tac gtt gaa   1349
Asp Phe Asp Asp Val Glu Val Lys Gly Phe Trp Gln Asp Tyr Val Glu
            430             435             440

aca ggc aaa gtg aaa gct gag gaa ttc ctt caa aac gta cgc caa acc   1397
Thr Gly Lys Val Lys Ala Glu Glu Phe Leu Gln Asn Val Arg Gln Thr
            445             450             455

agc cgt gat aac agc aga acc ccc ttc cag tgg gat gca agc aaa aac   1445
Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln Trp Asp Ala Ser Lys Asn
        460             465             470

gcg ggc ttt acc agt gga acc ccc tgg tta aaa atc aat ccc aat tat   1493
Ala Gly Phe Thr Ser Gly Thr Pro Trp Leu Lys Ile Asn Pro Asn Tyr
475             480             485             490
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```
aaa gaa atc aac agc gca gat cag att aat aat cca aat tcc gta ttt   1541
Lys Glu Ile Asn Ser Ala Asp Gln Ile Asn Asn Pro Asn Ser Val Phe
                495                     500                 505

aac tat tat aga aag ctg att aac att cgc cat gac atc cct gcc ttg   1589
Asn Tyr Tyr Arg Lys Leu Ile Asn Ile Arg His Asp Ile Pro Ala Leu
                510                     515                 520

acc tac ggc agt tat att gat tta gac cct gac aac aat tca gtc tat   1637
Thr Tyr Gly Ser Tyr Ile Asp Leu Asp Pro Asp Asn Asn Ser Val Tyr
                525                     530                 535

gct tac acc cga acg ctc ggc gct gaa aaa tat ctt gtg gtc att aat   1685
Ala Tyr Thr Arg Thr Leu Gly Ala Glu Lys Tyr Leu Val Val Ile Asn
                540                     545                 550

ttt aaa gaa gaa gtg atg cac tac acc ctg ccc ggg gat tta tcc atc   1733
Phe Lys Glu Glu Val Met His Tyr Thr Leu Pro Gly Asp Leu Ser Ile
555                     560                     565                 570

aat aag gtg att act gaa aac aac agt cac act att gtg aat aaa aat   1781
Asn Lys Val Ile Thr Glu Asn Asn Ser His Thr Ile Val Asn Lys Asn
                575                     580                 585

gac agg caa ctc cgt ctt gaa ccc tgg cag tcg ggc att tat aaa ctt   1829
Asp Arg Gln Leu Arg Leu Glu Pro Trp Gln Ser Gly Ile Tyr Lys Leu
                590                     595                 600

aat ccg taggtcgac                                                 1844
Asn Pro

<210> 14
<211> 604
<212> PRT
<213> Artificial sequence
<223> Description of the artificial sequence: coding for
      fusion protein of signal peptide from proteinase
      inhibitor I and sucrose isomerase from Erwinia
      rhapontici

<400> 14
Met Asp Val His Lys Glu Val Asn Phe Val Ala Tyr Leu Leu Ile Val
1               5                   10                  15

Leu Gly Leu Leu Val Leu Val Ser Ala Met Glu His Val Asp Ala Lys
                20                  25                  30

Ala Cys Thr Glu Leu Gly Ile Leu Thr Val Gln Gln Ser Asn Ala Leu
            35                  40                  45

Pro Thr Trp Trp Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser
        50                  55                  60

Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile
65                  70                  75                  80

Glu Asn Leu Asp Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile
                85                  90                  95

Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg
                100                 105                 110

Asp Tyr Arg Lys Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp
            115                 120                 125

Arg Leu Ile Ser Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp
            130                 135                 140

Ile Val Ile Asn His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser
145                 150                 155                 160
```

Lys Ser Gly Lys Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp
            165   170   175

Gly Lys Asp Gly His Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly
          180   185   190

Ser Ala Trp Glu Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr
          195   200   205

Phe Ala Lys Gln Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg
210   215   220

Gln Asp Leu Tyr Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser
225   230   235   240

Gly Leu Arg Phe Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe
          245   250   255

Pro Asp Leu Ser Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr
          260   265   270

Lys Gly Pro Lys Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val
          275   280   285

Leu Ser His Tyr Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro
          290   295   300

Leu Asp Lys Ser Ile Lys Phe Phe Asp Arg Arg Arg Asn Glu Leu Asn
305   310   315   320

Ile Ala Phe Thr Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu
              325   330   335

Arg Trp Arg Arg Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val
          340   345   350

Asp Lys Val Asp Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe
          355   360   365

Leu Asp Asn His Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp
          370   375   380

Arg Pro Gln Trp Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr
385   390   395   400

Leu Thr Gln Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly
          405   410   415

Met Thr Asn Tyr Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu
          420   425   430

Val Lys Gly Phe Trp Gln Asp Tyr Val Glu Thr Gly Lys Val Lys Ala
          435   440   445

Glu Glu Phe Leu Gln Asn Val Arg Gln Thr Ser Arg Asp Asn Ser Arg
          450   455   460

Thr Pro Phe Gln Trp Asp Ala Ser Lys Asn Ala Gly Phe Thr Ser Gly
465   470   475   480

Thr Pro Trp Leu Lys Ile Asn Pro Asn Tyr Lys Glu Ile Asn Ser Ala
          485   490   495

Asp Gln Ile Asn Asn Pro Asn Ser Val Phe Asn Tyr Tyr Arg Lys Leu
          500   505   510

Ile Asn Ile Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Ser Tyr Ile
          515   520   525

Asp Leu Asp Pro Asp Asn Asn Ser Val Tyr Ala Tyr Thr Arg Thr Leu
          530   535   540

```
Gly Ala Glu Lys Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met
545             550             555             560

His Tyr Thr Leu Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu
            565             570             575

Asn Asn Ser His Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu
            580             585             590

Glu Pro Trp Gln Ser Gly Ile Tyr Lys Leu Asn Pro
        595             600
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<210> 15
<211> 2477
<212> DNA
<213> Klebsiella sp.

<220>
<221> CDS
<222> (214)..(2007)
<223> coding for sucrose isomerase

<400> 15
gatatcactg gtattatgga gtattatact ccccccttat ttactcatca aagccaggcg 60

ttccactctg cctccggtat ataactttcc gggaaacaat cccttcctga aataattat  120

tgttaccgga gtcatactct ggctattgat gatttacgct tttctttaat aacaattcgt 180

ctcattcaca actgactttg caaggaaatt att atg tct ttt gtt acg cta cgt 234
                                    Met Ser Phe Val Thr Leu Arg
                                    1             5

acc ggg gtg gct gtc gcg ctg tca tct ttg ata ata agt ctg gcc tgc 282
Thr Gly Val Ala Val Ala Leu Ser Ser Leu Ile Ile Ser Leu Ala Cys
        10              15              20

ccg gct gtc agt gct gca cca tcc ttg aat cag gat att cac gtt caa 330
Pro Ala Val Ser Ala Ala Pro Ser Leu Asn Gln Asp Ile His Val Gln
    25              30              35

aag gaa agt gaa tat cct gca tgg tgg aaa gaa gct gtt ttt tat cag 378
Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln
40              45              50              55

atc tat cct cgc tca ttt aaa gac acc aat gat gat ggc att ggc gat 426
Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp
                60              65              70

att cgc ggt att att gaa aag ctg gac tat ctg aaa tcg ctc ggt att 474
Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile
            75              80              85

gac gct atc tgg atc aat ccc cat tac gac tct ccg aac acc gat aac 522
Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn
            90              95              100

ggc tat gac atc agt aat tat cgt cag ata atg aaa gag tat ggc aca 570
Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys Glu Tyr Gly Thr
        105             110             115

atg gag gat ttt gat agc ctt gtt gcc gaa atg aaa aaa cga aat atg 618
Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys Lys Arg Asn Met
120             125             130             135

cgc tta atg atc gac gtg gtc att aac cat acc agt gat caa cac ccg 666
Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro
            140             145             150
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tgg ttt att cag agt aaa agc gat aaa aac aac cct tat cgt gac tat     714
Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro Tyr Arg Asp Tyr
            155             160             165

tat ttc tgg cgt gac gga aaa gat aat cag cca cct aat aat tac ccc     762
Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro Asn Asn Tyr Pro
            170             175             180

tca ttt ttc ggc ggc tcg gca tgg caa aaa gat gca aag tca gga cag     810
Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala Lys Ser Gly Gln
            185             190             195

tac tat tta cac tat ttt gcc aga cag caa cct gat ctc aac tgg gat     858
Tyr Tyr Leu His Tyr Phe Ala Arg Gln Gln Pro Asp Leu Asn Trp Asp
200             205             210             215

aac ccg aaa gta cgt gag gat ctt tac gca atg ctc cgc ttc tgg ctg     906
Asn Pro Lys Val Arg Glu Asp Leu Tyr Ala Met Leu Arg Phe Trp Leu
                220             225             230

gat aaa ggc gtt tca ggc atg cga ttt gat acg gtg gca act tat tcc     954
Asp Lys Gly Val Ser Gly Met Arg Phe Asp Thr Val Ala Thr Tyr Ser
                235             240             245

aaa atc ccg gga ttt ccc aat ctg aca cct gaa caa cag aaa aat ttt    1002
Lys Ile Pro Gly Phe Pro Asn Leu Thr Pro Glu Gln Gln Lys Asn Phe
            250             255             260

gct gaa caa tac acc atg ggg cct aat att cat cga tac att cag gaa    1050
Ala Glu Gln Tyr Thr Met Gly Pro Asn Ile His Arg Tyr Ile Gln Glu
            265             270             275

atg aac cgg aaa gtt ctg tcc cgg tat gat gtg gcc acc gcg ggt gaa    1098
Met Asn Arg Lys Val Leu Ser Arg Tyr Asp Val Ala Thr Ala Gly Glu
280             285             290             295

att ttt ggc gtc ccg ctg gat cgt tcg tcg cag ttt ttt gat cgc cgc    1146
Ile Phe Gly Val Pro Leu Asp Arg Ser Ser Gln Phe Phe Asp Arg Arg
                300             305             310

cga cat gag ctg aat atg gcg ttt atg ttt gac ctc att cgt ctc gat    1194
Arg His Glu Leu Asn Met Ala Phe Met Phe Asp Leu Ile Arg Leu Asp
            315             320             325

cgc gac agc aat gaa cgc tgg cgt cac aag tcg tgg tcg ctc tct cag    1242
Arg Asp Ser Asn Glu Arg Trp Arg His Lys Ser Trp Ser Leu Ser Gln
            330             335             340

ttc cgc cag atc atc agc aaa atg gat gtc acg gtc gga aag tat ggc    1290
Phe Arg Gln Ile Ile Ser Lys Met Asp Val Thr Val Gly Lys Tyr Gly
345             350             355

tgg aac acg ttc ttc tta gat aac cat gac aac ccc cgt gcg gta tct    1338
Trp Asn Thr Phe Phe Leu Asp Asn His Asp Asn Pro Arg Ala Val Ser
360             365             370             375

cac ttc ggg gat gac agg ccg caa tgg cgg gag gcg tcg gct aag gca    1386
His Phe Gly Asp Asp Arg Pro Gln Trp Arg Glu Ala Ser Ala Lys Ala
            380             385             390

ctg gcg acg att acc ctc act cag cgg gcg acg ccg ttt att tat cag    1434
Leu Ala Thr Ile Thr Leu Thr Gln Arg Ala Thr Pro Phe Ile Tyr Gln
            395             400             405

ggt tca gag ctg gga atg act aat tat ccc ttc agg caa ctc aac gaa    1482
Gly Ser Glu Leu Gly Met Thr Asn Tyr Pro Phe Arg Gln Leu Asn Glu
            410             415             420
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ttt gac gac atc gag gtc aaa ggt ttc tgg cag gat tat gtc cag agt    1530
Phe Asp Asp Ile Glu Val Lys Gly Phe Trp Gln Asp Tyr Val Gln Ser
    425             430             435

gga aaa gtc acg gcc aca gag ttt ctc gat aat gtg cgc ctg acg agc    1578
Gly Lys Val Thr Ala Thr Glu Phe Leu Asp Asn Val Arg Leu Thr Ser
440             445             450             455

cgc gat aac agc aga aca cct ttc cag tgg aat gac acc ctg aat gct    1626
Arg Asp Asn Ser Arg Thr Pro Phe Gln Trp Asn Asp Thr Leu Asn Ala
                460             465             470

ggt ttt act cgc gga aag ccg tgg ttt cac atc aac cca aac tat gtg    1674
Gly Phe Thr Arg Gly Lys Pro Trp Phe His Ile Asn Pro Asn Tyr Val
            475             480             485

gag atc aac gcc gaa cgc gaa gaa acc cgc gaa gat tca gtg ctg aat    1722
Glu Ile Asn Ala Glu Arg Glu Glu Thr Arg Glu Asp Ser Val Leu Asn
        490             495             500

tac tat aaa aaa atg att cag cta cgc cac cat atc cct gct ctg gta    1770
Tyr Tyr Lys Lys Met Ile Gln Leu Arg His His Ile Pro Ala Leu Val
    505             510             515

tat ggc gcc tat cag gat ctt aat cca cag gac aat acc gtt tat gcc    1818
Tyr Gly Ala Tyr Gln Asp Leu Asn Pro Gln Asp Asn Thr Val Tyr Ala
520             525             530             535

tat acc cga acg ctg ggt aac gag cgt tat ctg gtc gtg gtg aac ttt    1866
Tyr Thr Arg Thr Leu Gly Asn Glu Arg Tyr Leu Val Val Val Asn Phe
                540             545             550

aag gag tac ccg gtc cgc tat act ctc ccg gct aat gat gcc atc gag    1914
Lys Glu Tyr Pro Val Arg Tyr Thr Leu Pro Ala Asn Asp Ala Ile Glu
            555             560             565

gaa gtg gtc att gat act cag cag cag gcg gct gcg ccg cac agc aca    1962
Glu Val Val Ile Asp Thr Gln Gln Gln Ala Ala Ala Pro His Ser Thr
        570             575             580

tcc ctg tca ttg agc ccc tgg cag gca ggt gtg tat aag ctg cgg        2007
Ser Leu Ser Leu Ser Pro Trp Gln Ala Gly Val Tyr Lys Leu Arg
    585             590             595

taatcacctg ggggattgat gacaagttcc ccagacaata gagttttcca ggtctttagc 2067
actgctgtgc tcagcgatag ttgtgctctc ctgtgacttc gtaagtgcct gtctcatggc 2127
aggcattgtc aggtcagaag ccttctcagg cagcctcgag taacagcgcc cagttagcat 2187
cccccctgaaa gatggggggt atgtataaat tagcgttaaa gaacatgaac cagccaccgt 2247
catcttatca accaacaggc gagatgagct ccgattcctg attcttcaca ttgccgttga 2307
tgcgcctgaa gcctcgccct ttagggccgg gaaataagca cagcatctgg cgatctcttt 2367
tgccacttta ctgatcacat ccggcctcat ccatttccgg gcggcttcag ccatcaggag 2427
aaagggtagt ggtcgtgtat atgagccagg ccaaaaaaag gtgtgatatc            2477
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<210> 16
<211> 598
<212> PRT
<213> Klebsiella sp.

<400> 16

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Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser
 1               5               10              15

Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu
            20              25              30
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Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp
          35   40   45

Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr
          50   55   60

Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp
65   70   75   80

Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
              85   90   95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
              100   105   110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala
          115   120   125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130   135   140

His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
145   150   155   160

Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn
              165   170   175

Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
              180   185   190

Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
          195   200   205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr
    210   215   220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe
225   230   235   240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr
              245   250   255

Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn
              260   265   270

Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr
    275   280   285

Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser
    290   295   300

Ser Gln Phe Phe Asp Arg Arg Arg His Glu Leu Asn Met Ala Phe Met
305   310   315   320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His
              325   330   335

Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp
              340   345   350

Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His
          355   360   365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
370   375   380

Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg
385   390   395   400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
              405   410   415

```
Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420                 425             430
Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu
            435                 440             445
Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
            450                 455             460
Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe
465                 470             475                 480
His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr
                485                 490             495
Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg
            500                 505             510
His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro
            515                 520             525
Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg
    530                 535             540
Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu
545                 550             555                 560
Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln
                565                 570             575
Ala Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala
                580                 585             590
Gly Val Tyr Lys Leu Arg
            595
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<210> 17
<211> 1797
<212> DNA
<213> Klebsiella sp.

<220>
<221> CDS
<222> (1)..(1794)
<223> coding for sucrose isomerase

<400> 17
atg tct ttt gtt acg cta cgt acc ggg gtg gct gtc gcg ctg tca tct    48
Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser
  1               5                  10                  15

ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg    96
Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu
                20                  25                  30

aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg   144
Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp
            35                  40                  45

aaa gaa gct gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc   192
Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr
        50                  55                  60

aat gat gat ggc att ggc gat att cgc ggt att att gaa aag ctg gac   240
Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp
 65                  70                  75                  80

tat ctg aaa tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac   288
Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95
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gac tct ccg aac acc gat aac ggc tat gac atc agt aat tat cgt cag        336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
            100             105             110

ata atg aaa gag tat ggc aca atg gag gat ttt gat agc ctt gtt gcc        384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala
            115             120             125

gaa atg aaa aaa cga aat atg cgc tta atg atc gac gtg gtc att aac        432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
            130             135             140

cat acc agt gat caa cac ccg tgg ttt att cag agt aaa agc gat aaa        480
His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
145             150             155             160

aac aac cct tat cgt gac tat tat ttc tgg cgt gac gga aaa gat aat        528
Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn
                165             170             175

cag cca cct aat aat tac ccc tca ttt ttc ggc ggc tcg gca tgg caa        576
Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
                180             185             190

aaa gat gca aag tca gga cag tac tat tta cac tat ttt gcc aga cag        624
Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
            195             200             205

caa cct gat ctc aac tgg gat aac ccg aaa gta cgt gag gat ctt tac        672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr
            210             215             220

gca atg ctc cgc ttc tgg ctg gat aaa ggc gtt tca ggc atg cga ttt        720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe
225             230             235             240

gat acg gtg gca act tat tcc aaa atc ccg gga ttt ccc aat ctg aca        768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr
                245             250             255

cct gaa caa cag aaa aat ttt gct gaa caa tac acc atg ggg cct aat        816
Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn
                260             265             270

att cat cga tac att cag gaa atg aac cgg aaa gtt ctg tcc cgg tat        864
Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr
            275             280             285

gat gtg gcc acc gcg ggt gaa att ttt ggc gtc ccg ctg gat cgt tcg        912
Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser
290             295             300

tcg cag ttt ttt gat cgc cgc cga cat gag ctg aat atg gcg ttt atg        960
Ser Gln Phe Phe Asp Arg Arg Arg His Glu Leu Asn Met Ala Phe Met
305             310             315             320

ttt gac ctc att cgt ctc gat cgc gac agc aat gaa cgc tgg cgt cac       1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His
                325             330             335

aag tcg tgg tcg ctc tct cag ttc cgc cag atc atc agc aaa atg gat       1056
Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp
            340             345             350

gtc acg gtc gga aag tat ggc tgg aac acg ttc ttc tta gat aac cat       1104
Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His
            355             360             365
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gac aac ccc cgt gcg gta tct cac ttc ggg gat gac agg ccg caa tgg      1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370             375             380

cgg gag gcg tcg gct aag gca ctg gcg acg att acc ctc act cag cgg      1200
Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg
385             390             395             400

gcg acg ccg ttt att tat cag ggt tca gag ctg gga atg act aat tat      1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
            405             410             415

ccc ttc agg caa ctc aac gaa ttt gac gac atc gag gtc aaa ggt ttc      1296
Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420             425             430

tgg cag gat tat gtc cag agt gga aaa gtc acg gcc aca gag ttt ctc      1344
Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu
            435             440             445

gat aat gtg cgc ctg acg agc cgc gat aac agc aga aca cct ttc cag      1392
Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
    450             455             460

tgg aat gac acc ctg aat gct ggt ttt act cgc gga aag ccg tgg ttt      1440
Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe
465             470             475             480

cac atc aac cca aac tat gtg gag atc aac gcc gaa cgc gaa gaa acc      1488
His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr
            485             490             495

cgc gaa gat tca gtg ctg aat tac tat aaa aaa atg att cag cta cgc      1536
Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg
            500             505             510

cac cat atc cct gct ctg gta tat ggc gcc tat cag gat ctt aat cca      1584
His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro
            515             520             525

cag gac aat acc gtt tat gcc tat acc cga acg ctg ggt aac gag cgt      1632
Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg
    530             535             540

tat ctg gtc gtg gtg aac ttt aag gag tac ccg gtc cgc tat act ctc      1680
Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu
545             550             555             560

ccg gct aat gat gcc atc gag gaa gtg gtc att gat act cag cag cag      1728
Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln
            565             570             575

gcg gct gcg ccg cac agc aca tcc ctg tca ttg agc ccc tgg cag gca      1776
Ala Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala
            580             585             590

ggt gtg tat aag ctg cgg taa                                          1797
Gly Val Tyr Lys Leu Arg
            595
```

<210> 18
<211> 598
<212> PRT
<213> Klebsiella sp.

<400> 18

```
Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser
1               5               10              15
```

●   ●

Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu
            20   25   30

Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp
            35   40   45

Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr
    50   55   60

Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp
65   70   75   80

Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
            85   90   95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
            100   105   110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala
        115   120   125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130   135   140

His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
145   150   155   160

Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn
            165   170   175

Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180   185   190

Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
    195   200   205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr
    210   215   220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe
225   230   235   240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr
            245   250   255

Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn
            260   265   270

Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr
        275   280   285

Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser
    290   295   300

Ser Gln Phe Phe Asp Arg Arg Arg His Glu Leu Asn Met Ala Phe Met
305   310   315   320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His
            325   330   335

Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp
            340   345   350

Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His
        355   360   365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
    370   375   380

Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg
385   390   395   400

```
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
            405             410             415

Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420             425             430

Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu
            435             440             445

Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
        450             455             460

Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe
465             470             475             480

His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr
                485             490             495

Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg
            500             505             510

His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro
            515             520             525

Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg
        530             535             540

Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu
545             550             555             560

Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln
            565             570             575

Ala Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala
            580             585             590

Gly Val Tyr Lys Leu Arg
            595
```

<210> 19

<211> 471

<212> DNA

<213> Enterobacter sp.

<220>

<221> CDS

<222> (1)..(471)

<223> coding for fragment of sucrose isomerase

<400> 19

```
gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc aat gat gat      48
Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp
  1               5                   10                  15

ggc att ggc gat att cgc ggt att att gaa aag ctg gac tat ctg aaa      96
Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys
                20                  25                  30

tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac gac tct ccg     144
Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro
                35                  40                  45

aac acc gat aac ggc tat gac atc agt aat tat cgt cag ata atg aaa     192
Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys
        50                  55                  60

gag tat ggc aca atg gag gat ttt gat agc ctt gtt gcc gaa atg aaa     240
Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys
 65                  70                  75                  80
```

```
aaa cga aat atg cgc tta atg atc gac gtg gtc att aac cat acc agt    288
Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser
                85                   90                   95

gat caa cac ccg tgg ttt att cag agt aaa agc gat aaa aac aac cct    336
Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro
            100                  105                  110

tat cgt gac tat tat ttc tgg cgt gac gga aaa gat aat cag cca cct    384
Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro
            115                  120                  125

aat aat tac ccc tca ttt ttc ggc ggc tcg gca tgg caa aaa gat gca    432
Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala
        130                  135                  140

aag tca gga cag tac tat tta cac tat ttt gcc aga cag                471
Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
145                  150                  155
```

<210> 20
<211> 157
<212> PRT
<213> Enterobacter sp.

<400> 20

```
Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp
 1               5                   10                  15

Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys
            20                  25                  30

Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro
            35                  40                  45

Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys
        50                  55                  60

Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys
65                  70                  75                  80

Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser
                85                  90                  95

Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro
            100                 105                 110

Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro
            115                 120                 125

Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala
        130                 135                 140

Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln
145                 150                 155
```

<210> 21
<211> 1782
<212> DNA
<213> Pseudomonas mesoacidophila MX45

<220>
<221> CDS
<222> (1)..(1779)
<223> coding for sucrose isomerase

<400> 21
```
atg ctt atg aag aga tta ttc gcc gcg tct ctg atg ctt gct ttt tca    48
```

```
     Met Leu Met Lys Arg Leu Phe Ala Ala Ser Leu Met Leu Ala Phe Ser
      1               5                  10                  15

     agc gtc tcc tct gtg agg gct gag gag gcc gta aag ccg ggc gcg cca    96
     Ser Val Ser Ser Val Arg Ala Glu Glu Ala Val Lys Pro Gly Ala Pro
                      20                  25                  30

     tgg tgg aaa agt gct gtc ttc tat cag gtc tat ccg cgc tcg ttc aag   144
     Trp Trp Lys Ser Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys
                  35                  40                  45

     gat acc aac ggt gat ggg atc ggc gat ttc aaa gga ctg acg gag aag   192
     Asp Thr Asn Gly Asp Gly Ile Gly Asp Phe Lys Gly Leu Thr Glu Lys
              50                  55                  60

     ctc gac tat ctc aag ggg ctc ggc ata gac gcc atc tgg atc aat cca   240
     Leu Asp Tyr Leu Lys Gly Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro
     65                  70                  75                  80

     cat tac gcg tct ccc aac acc gat aat ggc tac gat atc agc gac tat   288
     His Tyr Ala Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asp Tyr
                      85                  90                  95

     cga gag gtc atg aag gaa tat ggg acg atg gag gac ttc gat cgt ctg   336
     Arg Glu Val Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu
                     100                 105                 110

     atg gct gag ttg aag aag cgc ggc atg cgg ctc atg gtt gat gtc gtg   384
     Met Ala Glu Leu Lys Lys Arg Gly Met Arg Leu Met Val Asp Val Val
                 115                 120                 125

     atc aac cat tcg agt gac caa cac gaa tgg ttc aag agc agc cgg gcc   432
     Ile Asn His Ser Ser Asp Gln His Glu Trp Phe Lys Ser Ser Arg Ala
             130                 135                 140

     tcc aaa gac aat ccc tac cgt gac tat tat ttc tgg cgt gac ggc aaa   480
     Ser Lys Asp Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys
     145                 150                 155                 160

     gac ggt cac gag cca aac aat tac cct tcc ttc ttc ggc ggt tcg gca   528
     Asp Gly His Glu Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala
                     165                 170                 175

     tgg gag aag gac ccc gta acc ggg caa tat tac ctg cat tat ttc ggt   576
     Trp Glu Lys Asp Pro Val Thr Gly Gln Tyr Tyr Leu His Tyr Phe Gly
                 180                 185                 190

     cgt cag cag cca gat ctg aac tgg gac acg ccg aag ctt cgc gag gaa   624
     Arg Gln Gln Pro Asp Leu Asn Trp Asp Thr Pro Lys Leu Arg Glu Glu
                 195                 200                 205

     ctc tat gcg atg ctg cgg ttc tgg ctc gac aag ggc gta tca ggc atg   672
     Leu Tyr Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met
     210                 215                 220

     cgg ttc gat acg gtg gct acc tac tcg aag aca ccg ggt ttc ccg gat   720
     Arg Phe Asp Thr Val Ala Thr Tyr Ser Lys Thr Pro Gly Phe Pro Asp
     225                 230                 235                 240

     ctg aca ccg gag cag atg aag aac ttc gcg gag gcc tat acc cag ggg   768
     Leu Thr Pro Glu Gln Met Lys Asn Phe Ala Glu Ala Tyr Thr Gln Gly
                     245                 250                 255

     ccg aac ctt cat cgt tac ctg cag gaa atg cac gag aag gtc ttc gat   816
     Pro Asn Leu His Arg Tyr Leu Gln Glu Met His Glu Lys Val Phe Asp
                     260                 265                 270

     cat tat gac gcg gtc acg gcc ggc gaa atc ttc ggc gct ccg ctc aat   864
     His Tyr Asp Ala Val Thr Ala Gly Glu Ile Phe Gly Ala Pro Leu Asn
                     275                 280                 285
```

```
caa gtg ccg ctg ttc atc gac agc cgg agg aaa gag ctg gat atg gct    912
Gln Val Pro Leu Phe Ile Asp Ser Arg Arg Lys Glu Leu Asp Met Ala
    290             295             300

ttc acc ttc gat ctg atc cgt tat gat cgc gca ctg gat cgt tgg cat    960
Phe Thr Phe Asp Leu Ile Arg Tyr Asp Arg Ala Leu Asp Arg Trp His
305             310             315             320

acc att ccg cgt acc tta gcg gac ttc cgt caa acg atc gat aag gtc   1008
Thr Ile Pro Arg Thr Leu Ala Asp Phe Arg Gln Thr Ile Asp Lys Val
            325             330             335

gac gcc atc gcg ggc gaa tat ggc tgg aac acg ttc ttc ctc ggc aat   1056
Asp Ala Ile Ala Gly Glu Tyr Gly Trp Asn Thr Phe Phe Leu Gly Asn
            340             345             350

cac gac aat ccc cgt gcg gta tcg cat ttt ggt gac gat cgg ccg caa   1104
His Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln
            355             360             365

tgg cgc gaa gcc tcg gcc aag gct ctg gcc acc gtc acc ttg acc cag   1152
Trp Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Val Thr Leu Thr Gln
    370             375             380

cga gga acg ccg ttc atc ttc caa gga gat gaa ctc gga atg acc aac   1200
Arg Gly Thr Pro Phe Ile Phe Gln Gly Asp Glu Leu Gly Met Thr Asn
385             390             395             400

tac ccc ttc aag acg ctg cag gac ttt gat gat atc nnn nnn nnn nnn   1248
Tyr Pro Phe Lys Thr Leu Gln Asp Phe Asp Asp Ile Xaa Xaa Xaa Xaa
            405             410             415

nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn   1296
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            420             425             430

nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnt gtg gcg ttg act   1344
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Ala Leu Thr
            435             440             445

agc cga gca aac gcc cgc acg ccc ttt caa tgg gat gac agt gct aat   1392
Ser Arg Ala Asn Ala Arg Thr Pro Phe Gln Trp Asp Asp Ser Ala Asn
    450             455             460

gcg gga ttc aca act ggc aag cct tgg cta aag gtc aat cca aac tac   1440
Ala Gly Phe Thr Thr Gly Lys Pro Trp Leu Lys Val Asn Pro Asn Tyr
465             470             475             480

act gag atc aac gcc gcg cgg gaa att ggc gat cct aaa tcg gtc tac   1488
Thr Glu Ile Asn Ala Ala Arg Glu Ile Gly Asp Pro Lys Ser Val Tyr
            485             490             495

agc ttt tac cgc aac ctg atc tca atc cgg cat gaa act ccc gct ctt   1536
Ser Phe Tyr Arg Asn Leu Ile Ser Ile Arg His Glu Thr Pro Ala Leu
            500             505             510

tcg acc ggg agc tat cgc gac atc gat ccg agt aat gcc gat gtc tat   1584
Ser Thr Gly Ser Tyr Arg Asp Ile Asp Pro Ser Asn Ala Asp Val Tyr
            515             520             525

gcc tat acg cgc agc cag gat ggc gag acc tat ctg gtc gta gtc aac   1632
Ala Tyr Thr Arg Ser Gln Asp Gly Glu Thr Tyr Leu Val Val Val Asn
            530             535             540

ttc aag gca gag cca agg agt ttc acg ctt ccg gac ggc atg cat att   1680
Phe Lys Ala Glu Pro Arg Ser Phe Thr Leu Pro Asp Gly Met His Ile
545             550             555             560
```

●   ●

```
gcc gaa acc ctg att gag agc agt tcg cca gca gct ccg gcg gcg ggg     1728
Ala Glu Thr Leu Ile Glu Ser Ser Ser Pro Ala Ala Pro Ala Ala Gly
            565                 570                 575

gct gca agc ctt gag ctg cag cct tgg cag tcc ggc atc tac aag gtg     1776
Ala Ala Ser Leu Glu Leu Gln Pro Trp Gln Ser Gly Ile Tyr Lys Val
            580                 585                 590

aag taa                                                              1782
Lys
```

<210> 22
<211> 593
<212> PRT
<213> Pseudomonas mesoacidophila MX45

<400> 22

```
Met Leu Met Lys Arg Leu Phe Ala Ala Ser Leu Met Leu Ala Phe Ser
 1               5                  10                  15

Ser Val Ser Ser Val Arg Ala Glu Glu Ala Val Lys Pro Gly Ala Pro
            20                  25                  30

Trp Trp Lys Ser Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys
            35                  40                  45

Asp Thr Asn Gly Asp Gly Ile Gly Asp Phe Lys Gly Leu Thr Glu Lys
         50                  55                  60

Leu Asp Tyr Leu Lys Gly Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro
 65                  70                  75                  80

His Tyr Ala Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asp Tyr
                 85                  90                  95

Arg Glu Val Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu
            100                 105                 110

Met Ala Glu Leu Lys Lys Arg Gly Met Arg Leu Met Val Asp Val Val
            115                 120                 125

Ile Asn His Ser Ser Asp Gln His Glu Trp Phe Lys Ser Ser Arg Ala
         130                 135                 140

Ser Lys Asp Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys
145                 150                 155                 160

Asp Gly His Glu Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala
                 165                 170                 175

Trp Glu Lys Asp Pro Val Thr Gly Gln Tyr Tyr Leu His Tyr Phe Gly
            180                 185                 190

Arg Gln Gln Pro Asp Leu Asn Trp Asp Thr Pro Lys Leu Arg Glu Glu
            195                 200                 205

Leu Tyr Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met
210                 215                 220

Arg Phe Asp Thr Val Ala Thr Tyr Ser Lys Thr Pro Gly Phe Pro Asp
225                 230                 235                 240

Leu Thr Pro Glu Gln Met Lys Asn Phe Ala Glu Ala Tyr Thr Gln Gly
                 245                 250                 255

Pro Asn Leu His Arg Tyr Leu Gln Glu Met His Glu Lys Val Phe Asp
                 260                 265                 270

His Tyr Asp Ala Val Thr Ala Gly Glu Ile Phe Gly Ala Pro Leu Asn
         275                 280                 285
```

Gln Val Pro Leu Phe Ile Asp Ser Arg Arg Lys Glu Leu Asp Met Ala
290   295   300

Phe Thr Phe Asp Leu Ile Arg Tyr Asp Arg Ala Leu Asp Arg Trp His
305   310   315   320

Thr Ile Pro Arg Thr Leu Ala Asp Phe Arg Gln Thr Ile Asp Lys Val
                325   330   335

Asp Ala Ile Ala Gly Glu Tyr Gly Trp Asn Thr Phe Phe Leu Gly Asn
                340   345   350

His Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln
                355   360   365

Trp Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Val Thr Leu Thr Gln
    370   375   380

Arg Gly Thr Pro Phe Ile Phe Gln Gly Asp Glu Leu Gly Met Thr Asn
385   390   395   400

Tyr Pro Phe Lys Thr Leu Gln Asp Phe Asp Asp Ile Xaa Xaa Xaa Xaa
                405   410   415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                420   425   430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Ala Leu Thr
                435   440   445

Ser Arg Ala Asn Ala Arg Thr Pro Phe Gln Trp Asp Asp Ser Ala Asn
    450   455   460

Ala Gly Phe Thr Thr Gly Lys Pro Trp Leu Lys Val Asn Pro Asn Tyr
465.   470   475   480

Thr Glu Ile Asn Ala Ala Arg Glu Ile Gly Asp Pro Lys Ser Val Tyr
                485   490   495

Ser Phe Tyr Arg Asn Leu Ile Ser Ile Arg His Glu Thr Pro Ala Leu
                500   505   510

Ser Thr Gly Ser Tyr Arg Asp Ile Asp Pro Ser Asn Ala Asp Val Tyr
                515   520   525

Ala Tyr Thr Arg Ser Gln Asp Gly Glu Thr Tyr Leu Val Val Val Asn
    530   535   540

Phe Lys Ala Glu Pro Arg Ser Phe Thr Leu Pro Asp Gly Met His Ile
545   550   555   560

Ala Glu Thr Leu Ile Glu Ser Ser Ser Pro Ala Ala Pro Ala Ala Gly
                565   570   575

Ala Ala Ser Leu Glu Leu Gln Pro Trp Gln Ser Gly Ile Tyr Lys Val
                580   585   590

Lys

<210> 23
<211> 1417
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> promoter
<222> (1)...(1417)
<223> promoter of lemmi9

```
<400> 23
ataatttaac catctagaga tccacaaatc atgtttccat atcatggtag tagttggtgc 60
tacgaagtat ctataaatta ttgagaaata cctggtggaa tcccaagtga aacggaaagg 120
cccttactta ttaaataaaa aaacatttga caatagaaaa ttgagaccaa tctgcatatg 180
aaacatcagg atccccacat ttcacaaatt ttacaagtta attaagccct actctgtcca 240
tatggaactt ttctgcactt ccacgcacca acgaatatgc tgaaaattga tgttttagat 300
gtgtacgaat aaagcaatca aagaacgcgg gcgcaacgcg cgctggagac actgccattc 360
atgtgtgcct aacgtgtttt cttttagtcat tacgctccta ctaccgactc aatatatatt 420
aactatagta ttttttatttt atgacgagaa acgtaatttt aaatgtagat atatttttaac 480
aagctatgat aattacatct tgttgccgta gtcataaatg acacaaatta aggtttgatt 540
ttcgtccact tctaagattt cttgttctaa tactagtata tttctgattt aaaaagttat 600
ttagtttttt ttgaattagc tgataaatgc caaaaactga aaattaaagt actttttaat 660
tttataaaaa taatatcatg gaaattaaaa cgagaaatta atgaaaagt agaagattgc 720
tttgccataa tatagtgtta cttttcgtat tatttttatta agcgtaaaat tacataaagg 780
tatccgtgct taaatttcta gcttgagagc attttttgaa gcaaagtttt cgataaatca 840
agtttttaata taaaattaca atcatcattt ctaattatat taattcttta aaaataaaat 900
taaaaaaata tatacaataa ttgaagctcg gataaattaa aatatgtaac tattaaatat 960
tactcggata tattaaatat tattcgatta tattaatatg tagctcaaaa tatattaaat 1020
aataatacaa atatattaat atatgtaaat catatacatt aaaaactatc ttaaatatat 1080
aatatgcagc tgtaatatat taacccagat acataagcac ctcgagtaca ttaaacaaat 1140
aaaagaattt aaaaataata aaaataagtg aaagcaataa attgtatatt tctataatttt 1200
atcccttttat taatactaaa taaagttaga gaacctaaac aggaagcaca attatgacac 1260
gaggagagaa tagcgcgtca attgtgaccc tttacgcgga agtatatgta ataaatagta 1320
gactctttttt ctatatttgt atatcccata acaagagcag agatattcgt ttagcacaaa 1380
acaggcatac tattcaattc cctttcgttc cagaagc 1417
```

```
<210> 24
<211> 374
<212> DNA
<213> Nicotiana tabacum
```

```
<220>
<221> promoter
<222> (1)..(374)
<223> promoter of delta-0.3TobRB7
```

```
<400> 24
agcttatcta aacaaagttt taaattcatt tcttaaacgt ccattacaat gtaatataac 60
ttagtcgtct caattaaacc attaatgtga aatataaatc aaaaaaagcc aaagggcggt 120
gggacggcgc caatcatttg tcctagtcca ctcaaataag gcccatggtc ggcaaaacca 180
aacacaaaat gtgttatttt taatttttttc ctctttttatt gttaaagttg caaaatgtgt 240
tatttttggt aagaccctat ggatatataa agacaggtta tgtgaaactt ggaaaaccat 300
caagttttaa gcaaaaccct cttaagaact taaattgagc ttcttttggg gcattttttct 360
agtgagaact aaaa 374
```

```
<210> 25
<211> 27
<212> DNA
<213> Artificial sequence
```

```
<220>
<223> Description of the artificial sequence:
      oligonucleotide primer
```

```
<400> 25
ggatccggta ccgttcagca atcaaat 27
```

```
<210> 26
<211> 23
<212> DNA
<213> Artificial sequence
```

```
<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 26
gtcgacgtct tgccaaaaac ctt                                    23

<210> 27
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 27
gtcgacctac gtgattaagt ttata                                  25

<210> 28
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 28
atcgaattca taatttaacc atctagag                               28

<210> 29
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 29
atcggtacct gcttctggaa cgaaaggg                               28

<210> 30
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 30
ggaattcagc ttatctaaac aaagttttaa attc                        34

<210> 31
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      oligonucleotide primer

<400> 31
gggtaccagt tctcactaga aaaatgcccc                             30

<210> 32
<211> 461
```

```
<212> DNA
<213> Wheat dwarf virus

<220>
<221> promoter
<222> (1)..(461)
<223> V-sense promoter from Wheat Dwarf Virus

<400> 32
ccggcaggtc cttagcgaaa aaacggggtg tgccagaaaa ctctatgctc taccctgcgt 60
ggaggtgtga attctgcaca ctgctaatgc aatgtgtcca atgctttata tagggcaggt 120
tttggcggga gaacagggcc cttgtgttcc cacgggagcg tagcgtatcg tgtgggccct 180
gttcggtgtg tggtcggggg gcctccacgc gggttataat attaccccgc gtggtggccc 240
ccgacgcgca ctcggctttt cgtgagtgcg cggaggcttt tggaccacat cttttctgac 300
cactttcgtg gaatatgttg atttatcaca cttttgacgc ggaaatctgt gccatgcctt 360
agcttataag gaagtgcgtg gtagcccatc tcgatggagc aggcaatagc ccccccgctt 420
cctatacggg actatcaata ccagacccct tccattcccg g                     461
```

```
<210> 33
<211> 1173
<212> DNA
<213> Maize streak virus

<220>
<221> promoter
<222> (1)..(1173)
<223> V-sense promotor from Maize Streak Virus

<400> 33
aagcttattt gcagagtatt caaaatactg caattttgtg gaccaatcaa agggaagctc 60
tttctggatc atggagaggt actcttcttt ggaagtagcg tgtgaaataa tgtctcgcat 120
tatttcatct ttagaaggct ttttttcctt tacctctgaa tcagattttc cgaggaaggg 180
ggacttccta ggaatgaaag tacctctctc aaacacagcc agaggttcct tgagaatgta 240
atccctcacc ctgtttactg acttggcact ctgaatattt gggtgaaacc catttatatc 300
aaagaacctt gagtcagata tccttaccgg cttctctgtc tgaagcaatg catgtaaatg 360
caaacttcca tctttatgtg cctctcgggc acatagaatg tatttgggaa tccaacgaac 420
aacgagctcc cagatcatct gacaggcgat ttcaggattt tctggacact ttggataggt 480
taggaacgtg ttagcgttcc ggtgtgagaa ctgacggttg gatgaggagg aggccattgc 540
cgacgacgga ggttgaggct gagggatggc agactgggag ctccaaactc tatagtatac 600
ccgtgcgcct tcgcctcgag gcgaaatccg ccgctccctt gtcttgtagt ggttgcaaat 660
gggccggacc gggccggccc agcaggaaaa gaaggcgcgc actaatatta ccgcgccttc 720
ttttcctgcg agggcccggt agggtcgacc ccgagcgatt tgatgtaaag tttggtcctg 780
ctttgtatga tttatctaaa gcagcccatt ctaaagaatc cggtcccggt cactataaat 840
tgcctaacaa gtgcgattca ttcatggatc cacagaacgc cctgtattat cagccgcggg 900
tacccacagc agctccgaca tccggaggag tgccgtggag tcgcgtaggc gaggtagcta 960
ttttgagctt tgttgcattg atttgctttt acctgcttta cctttgggtg ctgagagacc 1020
ttatcttagt tctgaaggct cgacaaggca gatccacgga ggagctgata tttggtggac 1080
aagctgtgga taggagcaac cctatcccta atataccagc accaccaagt cagggcaatc 1140
ccgggccatt tgttccatcg actctagtcg acc                              1173
```

```
<210> 34
<211> 353
<212> DNA
<213> Pepper huasteco virus

<220>
<221> promoter
<222> (1)...(353)
<223> V-sense promoter from Pepper huasteco virus

<400> 34
catatttgta ataagagagg tgtacaccga ttggagctct ttaacctggg cttattgtat 60
cggtgtattg gtagccaata tatagtatat gggagttatc taggatcttc gtacacgtga 120
```

```
gggccatccg ttataatatt accggatggc cgaccgctta ccttatctat ccgtactgct 180
ttatttgaat taaagatgtt acttttatgc tatccaatga agcgtagcgt ctgggaagct 240
tagttatcag ttccagacgt ggggaccaag tagtgtatga ccactttatt gactgtcagc 300
tttataaatt gaaattaaaa cataagtggt ccatgtacct ttaattcaaa atg 353
```

<210> 35
<211> 1803
<212> DNA
<213> Serratia plymuthica

<220>
<221> CDS
<222> (1)..(1800)
<223> coding for sucrose isomerase

<400> 35

```
atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca    48
Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
1               5                   10                  15

tca tta agc gtc tca tgc cag caa gcc tta ggt acg caa caa ccc ttg    96
Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu
            20                  25                  30

ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg   144
Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
        35                  40                  45

aag gag gct gtt ttt tat cag gtg tat ccg cgt tcc ttt aaa gac act   192
Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
    50                  55                  60

aac ggg gat ggt atc ggg gat att aaa ggc atc ata gaa aaa tta gac   240
Asn Gly Asp Gly Ile Gly Asp Ile Lys Gly Ile Ile Glu Lys Leu Asp
65                  70                  75                  80

tat tta aaa gct ttg ggg att gat gcc att tgg atc aac cca cat tat   288
Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85                  90                  95

gac tcc ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa   336
Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100                 105                 110

atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct   384
Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
        115                 120                 125

gaa atg aaa aaa cgt aac atg cgg ttg atg att gat gtg gtc atc aac   432
Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130                 135                 140

cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag   480
His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145                 150                 155                 160

gat aat cct tat cgt ggc tat tac ttc tgg aaa gat gct aaa gaa ggg   528
Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                165                 170                 175

cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa   576
Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180                 185                 190

aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa   624
Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
        195                 200                 205
```

```
cag cct gac cta aac tgg gat aac ccc aaa gtc cgt caa gat ctt tat    672
Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
    210              215              220

gca atg ttg cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgc ttt    720
Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225              230              235              240

gat acg gta gcg acc tac tca aaa att ccg gac ttc cca aat ctc acc    768
Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
              245              250              255

caa caa cag ctg aag aat ttt gca gct gag tat acc aag ggc cct aat    816
Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
          260              265              270

att cat cgt tac gtc aat gaa atg aat aga gaa gtt ttg tct cat tac    864
Ile His Arg Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
          275              280              285

gac att gcc act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg    912
Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
    290              295              300

ata aaa ttc ttc gat cgc cgt cgc gat gag ctg aac atc gca ttt acc    960
Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305              310              315              320

ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga   1008
Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
              325              330              335

aaa gag tgg aaa ttg tcg caa ttc cga cag gtc atc gat aac gtt gac   1056
Lys Glu Trp Lys Leu Ser Gln Phe Arg Gln Val Ile Asp Asn Val Asp
              340              345              350

cgt act gcc ggc gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac   1104
Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
          355              360              365

gac aat ccg cgc gct gtc tcc cac ttt ggc gat gat cgc cca caa tgg   1152
Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
          370              375              380

cgc gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa cga   1200
Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385              390              395              400

gca acg cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat tac   1248
Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
              405              410              415

ccc ttc aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt ttt   1296
Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
              420              425              430

tgg cat gac tac gtt gag aca gga aag gtg aaa gcc gac gag ttc ttg   1344
Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
              435              440              445

caa aat gta cgc ctg acg agc agg gat aac agc cgg aca ccg ttc caa   1392
Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
          450              455              460

tgg gat acg agc aaa aat gca gga ttc acg agc gga aaa cct tgg ttc   1440
Trp Asp Thr Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465              470              475              480
```

```
aag gtc aat cca aac tac cag gaa atc aat gcg gta agt caa gtc gca    1488
Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Ala
                485             490             495

cag ccc gac tcg gta ttt aat tat tat cgt cag ttg atc aag ata agg    1536
Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
                500             505             510

cat aac atc ccg gca ctg acc tat ggc aca tac acc gat ttg gat cct    1584
His Asn Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
                515             520             525

gca aat gat tcg gtc tac gcc tat aca cgc agc ctt ggg gcg gaa aaa    1632
Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
                530             535             540

tat ctt gtt gtc gtt aac ttc cag gaa caa gtg atg aga tat aaa tta    1680
Tyr Leu Val Val Val Asn Phe Gln Glu Gln Val Met Arg Tyr Lys Leu
545             550             555             560

ccg gat aat cta tcc atc gag aaa gtg att ata gaa agc aac agc aaa    1728
Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys
                565             570             575

aac gtt gtg aaa aag aat gat tcc tta ctc gaa cta aaa cca tgg cag    1776
Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
                580             585             590

tca ggg gtt tat aaa cta aat caa taa                                1803
Ser Gly Val Tyr Lys Leu Asn Gln
                595             600
```

<210> 36
<211> 600
<212> PRT
<213> Serratia plymuthica

<400> 36

```
Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr
1               5               10              15

Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu
                20              25              30

Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp
            35              40              45

Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr
        50              55              60

Asn Gly Asp Gly Ile Gly Asp Ile Lys Gly Ile Ile Glu Lys Leu Asp
65              70              75              80

Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
                85              90              95

Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys
            100             105             110

Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser
        115             120             125

Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn
    130             135             140

His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys
145             150             155             160

Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly
                165             170             175
```

```
Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln
            180                 185             190

Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln
            195                 200             205

Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr
            210             215             220

Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe
225             230             235             240

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr
            245                 250             255

Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn
            260                 265             270

Ile His Arg Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr
            275                 280             285

Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser
    290                 295             300

Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr
305             310             315                 320

Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg
            325             330             335

Lys Glu Trp Lys Leu Ser Gln Phe Arg Gln Val Ile Asp Asn Val Asp
            340             345             350

Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His
            355             360             365

Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp
370             375             380

Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg
385             390             395                 400

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr
            405             410             415

Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe
            420             425             430

Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu
            435             440             445

Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln
450             455             460

Trp Asp Thr Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe
465             470             475             480

Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Ala
            485             490             495

Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg
            500             505             510

His Asn Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro
    515             520             525

Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys
    530             535             540

Tyr Leu Val Val Val Asn Phe Gln Glu Gln Val Met Arg Tyr Lys Leu
545             550             555             560
```

50

Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys
                565   570   575

Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln
                580   585   590

Ser Gly Val Tyr Lys Leu Asn Gln
            595   600